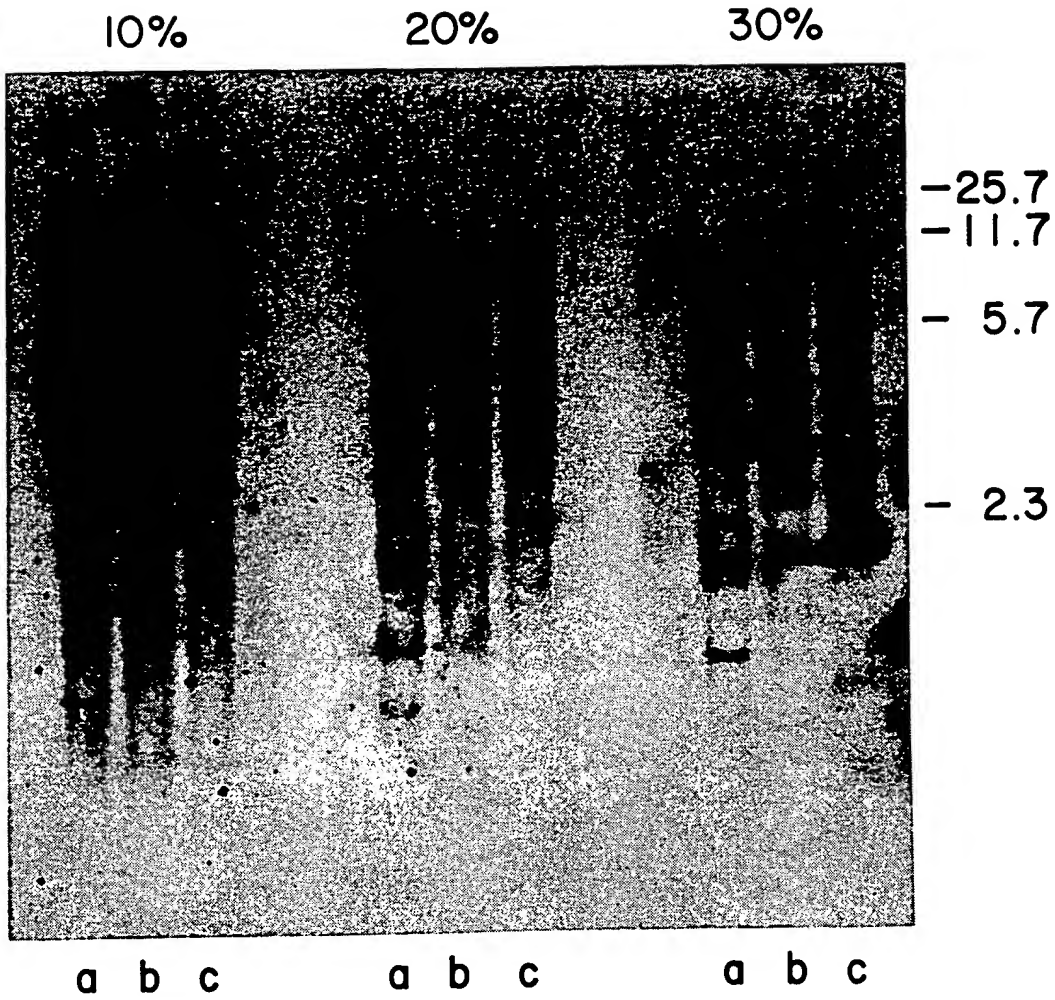
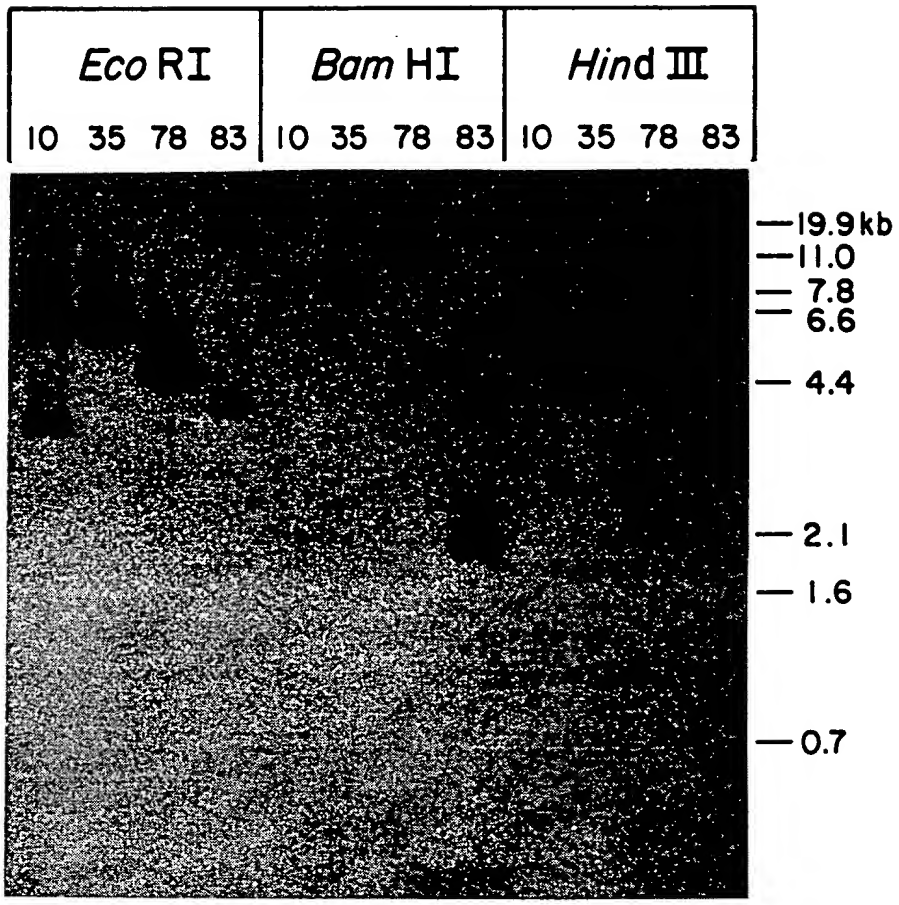


Fig. 13


Eco RI
Bam HI
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10 35 78 83
10 35 78 83
19.9kb
11.0
7.8
6.6
4.4
2.1
1.6
0.7

Fig. 8

GGATCCACAGCATAAATGTGTTGTCACAATTTCACGGTGGGGGTAATTAGGAAAAAAAAAATCTCAGAAGAACTGTCAATAGGGGAAGGGGGGCAATAATGAAAACAACGTTTGCGAA
50 100

ATGCTGTCCTAACCCATTTGAAGAGTACAAACTGAAAAACAAAAACAAAAGTAGAAAGCAAGAGGGAACTTTCAGAAAATGGAAACCATGGACTCCTATTTAAGACACAGACCTGAAGG
150 200

S1 S10
met ala pro ala trp ser leu leu leu ala
AAGGTCTTCAGAGAACCTAGAAAGCAGGTTCACAGAGTCACCCACCGCCCCAGGCCACAAGCATCTTCAAGGTCCCCG ATG GCC CCA GCC TGG TCC CTC CTC CTG GCT
250 300

S20 S23 1 10
leu leu leu leu ser cys asn ala ile cys ser leu gly CYS HIS LEU PRO HIS SER HIS SER LEU ALA LYS ARG ARG VAL LEU THR LEU
CTG CTG CTG CTC AGC TGC AAC GCC ATC TGC TCT CTG GGC TGC CAC CTG CCT CAC TCC CAC AGC CTG GCC AAG AGG AGA GTC CTG ACA CTC
350 400

20 30 40
LEU ARG GLN LEU ARG ARG VAL SER PRO SER SER CYS LEU GLN ASP ARG ASN ASP PHE ALA PHE PRO GLN GLU ALA LEU GLY GLY SER GLN
CTG CGA CAA CTG AGG AGG GTC TCC CCT TCC TCC TGC CTG CAG GAC AGA AAT GAC TTC GCA TTC CCC CAG GAG GCG CTG GGT GGC AGC CAG
450 500

50 60 70
LEU GLN LYS ALA GLN ALA ILE SER VAL LEU HIS GLU VAL THR GLN HIS THR PHE GLN LEU PHE SER THR GLU GLY SER ALA ALA VAL TRP
TTG CAG AAG GCT CAA GCC ATC TCT GTA CTC CAC GAG GTG ACC CAA CAC ACC TTC CAG CTT TTC AGC ACA GAG GGC TCG GCC GCT GTG TGG
550 600

80 90 100
ASP GLU SER LEU LEU ASP LYS LEU ARG THR ALA LEU ASP GLN GLN LEU THR ASP LEU GLN ALA CYS LEU ARG GLN GLU GLU GLY LEU PRO
GAT GAG AGC CTC CTG GAC AAG CTC CGC ACT GCA CTG GAT CAG CAG CTC ACT GAC CTG CAA GCC TGT CTG AGG CAG GAG GAG GGG CTG CCA
650 700

110 120 130
GLY ALA PRO LEU LEU LYS GLU ASP SER SER LEU ALA VAL ARG LYS TYR PHE HIS ARG LEU THR LEU TYR LEU GLN GLU LYS ARG HIS SER
GGG GCT CCC CTG CTC AAG GAG GAC TCC AGC CTG GCT GTG AGG AAA TAC TTC CAC AGA CTC ACT CTC TAT CTG CAA GAG AAG AGA CAC AGC
750

140 150 160 166Stop
PRO CYS ALA TRP GLU VAL VAL ARG ALA GLN VAL MET ARG ALA PHE SER SER SER THR ASN LEU GLN GLU ARG PHE ARG ARG LYS ASP OP
CCT TGT GCC TGG GAG GTT GTC AGA GCA CAA GTC ATG AGA GCC TTC TCT TCC TCA ACA AAC TTG CAG GAG AGA TTC AGG AGA AAG GAC TGA
800 850

CACACACCTGGTTCAACACGGAAATGATTCTCACGGACCAACAGACCACACTTCCTCCTGCGCTGCCATGTGGAAGACTCATTTCTGCTGTCATCAGGCACTGAACTGAATCAATTTGTT
900 950 1000

AAATGATTTCAGGTATATTATGTGACATCATGATCTACTCTACAGGCACTACTCTGTCCCAGATACTCAAGCTAATCCATCTACTTATTTATCTATTTGGTATTTATTTATCTAATTTAA
1050 1100

TATTTATTTATCTATATATAAAGAATTAAATTATTTTGTTCATATAATTATGTATGTATAATTAATGGAAAAATATATTTTGTATTTAGTCAATTTATGAGTTTTCTTCATTCATTAAAC
1150 1200

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1250 1300 1350

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1400 1450

F I G U R E ~~3a~~ 15A

BoIFN-α2

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GGGCTCCTATTTAAGACACAGGCCTGAAGGAAGGTCTTCAGAGAATCTAGAGAGCAGGTTCACAGAGTCACCCACTGCC

                                S1                                        S10
                                met ala pro ala trp ser phe leu leu ala leu leu
CCAGGGCAGAAGCATCTGCAAGGTCCCCG   ATG GCC CCA GCC TGG TCC TTC CTC CTG GCC CTG CTG

                              S20         S23   1
leu leu ser cys asn ala ile cys ser leu gly cys his leu pro his thr his ser leu
CTG CTC AGC TGC AAC GCC ATC TGC TCT TTG GGT TGC CAC CTG CCT CAC ACC CAC AGC CTG

 10                                        20
pro asn arg arg val leu thr leu leu arg gln leu arg arg val ser pro ser ser cys
CCC AAC AGG AGG GTC CTG ACA CTC CTG CGA CAA CTG AGG AGG GTC TCC CCT TCC TCC TGC

 30                                        40
leu gln asp arg asn asp phe ala phe pro gln glu ala leu gly gly ser gln leu gln
CTG CAG GAC AGA AAT GAC TTT GCA TTC CCC CAG GAG GCG CTG GGT GGC AGC CAG TTG CAG

 50                                        60
lys ala gln ala ile ser val leu his glu val thr gln his thr phe gln leu phe ser
AAG GCT CAA GCC ATC TCT GTG CTC CAC GAG GTG ACC CAG CAC ACC TTC CAG CTC TTC AGC

 70                                        80
thr glu gly ser ala ala val trp asp gln ser leu leu asp lys leu arg ala ala leu
ACA GAG GGC TCG GCC GCT GTG TGG GAC CAG AGC CTC CTG GAC AAG CTC CGA GCT GCA CTG

 90                                       100
asp gln gln leu thr asp leu gln ala cys leu arg gln glu glu gly leu arg gly ala
GAT CAG CAG CTC ACT GAC CTG CAA GCC TGT CTG AGG CAG GAG GAG GGG CTG CGA GGG GCT

110                                       120
pro leu leu lys glu asp ala ser leu ala val arg lys tyr phe his arg leu thr leu
CCC CTG CTC AAG GAG GAT GCC AGC CTG GCT GTG AGG AAA TAC TTC CAC AGA CTC ACT CTC

130                                       140
tyr leu gln glu lys arg his ser pro cys ala trp glu val val arg ala glu val met
TAT CTG CAA GAG AAG AGA CAC AGC CCT TGT GCC TGG GAG GTT GTC AGA GCA GAA GTC ATG

150                                       160                   166
arg ala phe ser ser ser thr asn leu gln glu lys phe arg arg lys asp OP
AGA GCC TTC TCT TCT TCA ACA AAC TTG CAG GAG AAA TTC AGG AGA AAG GAC TGA CACACA

CCTGGTTCAACACGGAAATGATTCTCATGGACCAACAGACCACACTTCCTCCTGCACTGCCATGTGGAAGACTCTCAT

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GATTTGATGAATTC
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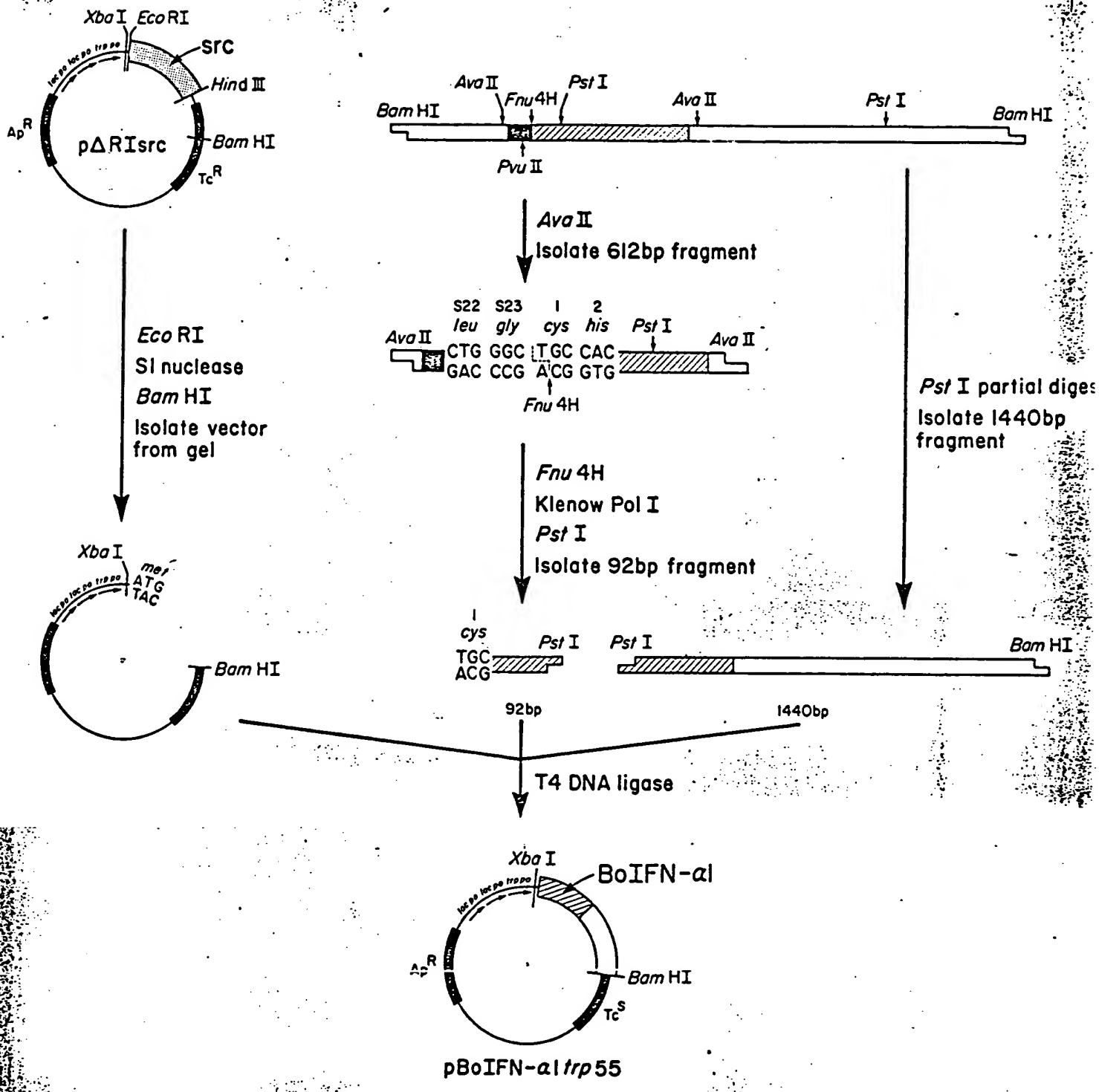
FIGURE 5b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Hind III
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pΔRIsrc
Bam HI
Tc^R
Ava II
Fnu 4H
Pst I
Ava II
Pst I
Bam HI
Bam HI
Pvu II
Ava II
Isolate 612bp fragment
S22 S23 1 2
leu gly cys his
Ava II
CTG GGC TGC CAC
GAC CCG ACG GTG
Pst I
Ava II
Fnu 4H
Eco RI
S1 nuclease
Bam HI
Isolate vector from gel
Pst I partial dige
Isolate 1440bp fragment
Fnu 4H
Klenow Pol I
Pst I
Isolate 92bp fragment
Xba I
met
ATG
TAC
Bam HI
1
cys
TGC
ACG
Pst I
Pst I
Bam HI
92bp
1440bp
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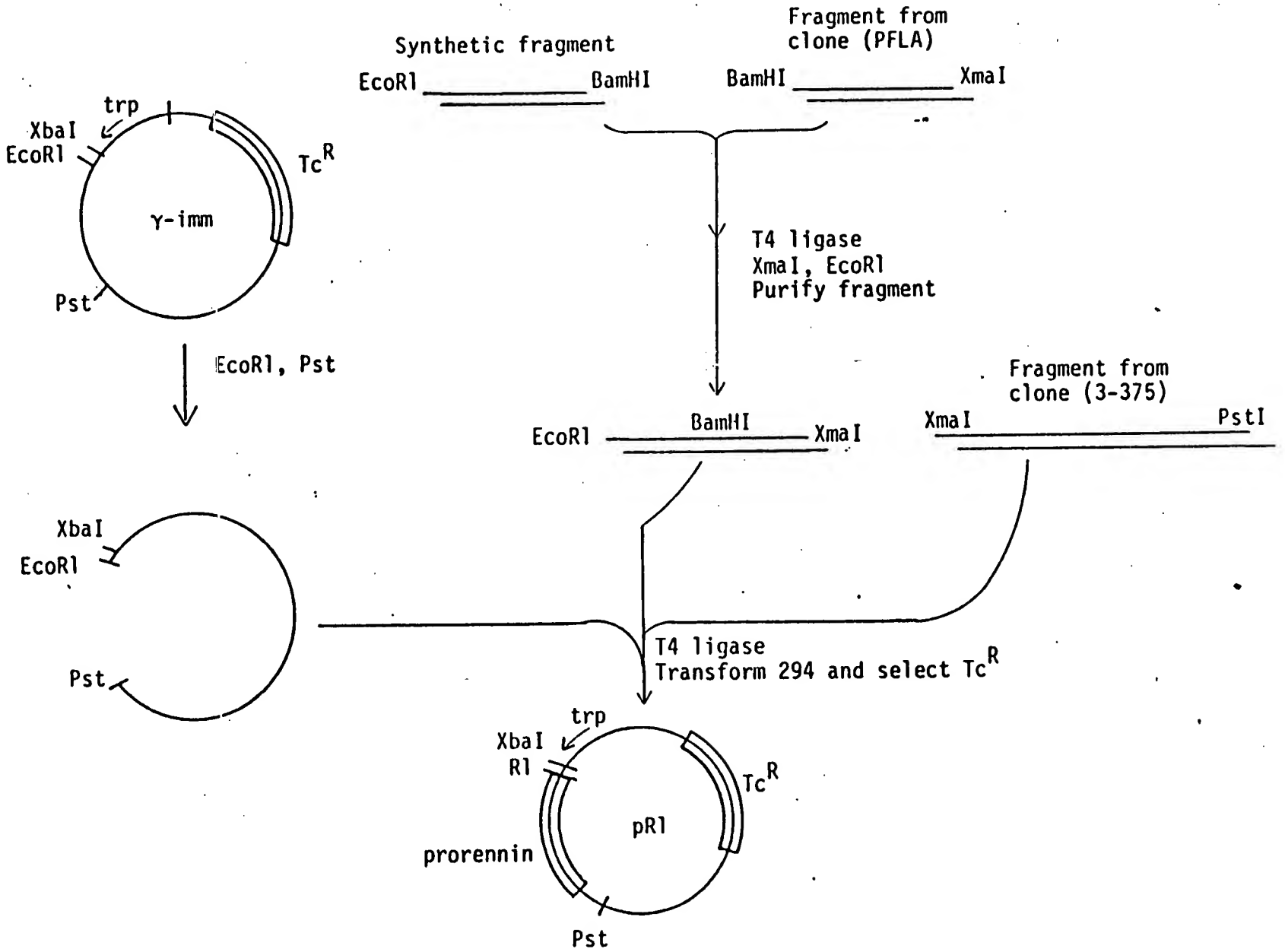
Xba I
BoIFN-α1
Ap^R
Bam HI
Tc^S
pBoIFN-α1trp55

FIGURE 16

Figure 17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BamHI
Fragment from clone (PFLA)
BamHI
XmaI
trp
XbaI
EcoRl
Tc^R
γ-imm
Pst
T4 ligase
XmaI, EcoRl
Purify fragment
EcoRl, Pst
Fragment from clone (3-375)
XmaI
PstI
EcoRl
BamHI
XmaI
XbaI
EcoRl
Pst
T4 ligase
Transform 294 and select Tc^R
trp
XbaI
Rl
Tc^R
pRl
prorennin
Pst